#10/B

SEQUENCE LISTING

<110> Stewart, A. F.
Zhang, Y.
Hallet, B.

<120> A New Tyrosine Recombinase for Genetic Engineering

<130> 9882-012-999

<140> 09/895,435
<141> 2001-06-30

<160> 10

<170> PatentIn version 3.0

<210> 1
<211> 244
<212> DNA
<213> Bacillus thuringiensis

<400> 1
ggtaccgcca gcatttcgga aaaaaaccac gctaagaaaa tcagagttaa aaaatcagaa 60
aatatatcat tattccttga cacatacatg ttctttttt atacaaaaaa taatacaaca 120
caatattaat tgtgttgtat taggtgttat aataaatata aatctagggg tttaacgcaa 180
cacaatttat cgataaataa atacttttag acgcaacaca atttatagac gcggaggaaa 240
tcac 244

<210> 2
<211> 118
<212> DNA
<213> Bacillus thuringiensis

B1

<400> 2
taatacaaca caatattaat tgtgttgtat taggtgttat aataaatata aatctagggg 60
tttaacgcaa cacaatttat cgataaataa atacttttag acgcaacaca atttatag 118

<210> 3
<211> 32
<212> DNA
<213> Bacillus thuringiensis

<400> 3
taatacaaca caatattaat tgtgttgtat ta 32

<210> 4
<211> 249
<212> DNA
<213> Bacillus thuringiensis

<400> 4
ggggtaccgc cagcatttcg gaaaaaaacc acgctaagaa aatcagagtt aaaaaatcag 60
aaaatatatc attattcctt gacacataca tgttcttttt ttatacaaaa aataatacaa 120
cacaatatta attgtgttgt attaggtgtt ataataaata taaatctagg ggtttaacgc 180
aacacaattt atcgataaat aaatactttt agacgcaaca caatttatag acgcggagga 240
aatcacatg 249

<210> 5
<211> 798

<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)..(798)

<400> 5

```
atg gat gtt gca aaa cag ttt tct tct tat ctt aaa caa gag aat aaa        48
Met Asp Val Ala Lys Gln Phe Ser Ser Tyr Leu Lys Gln Glu Asn Lys
1               5                  10                  15
acc gag aac act gtt cag gga tac aca tca ggt att aga cag tac ata        96
Thr Glu Asn Thr Val Gln Gly Tyr Thr Ser Gly Ile Arg Gln Tyr Ile
            20                  25                  30
aaa tgg ttt gaa ggt tcc tat gac aga aaa ttg aca aaa ttg tac cga       144
Lys Trp Phe Glu Gly Ser Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg
        35                  40                  45
caa aat atc tta gag tac att agt tat tta aag aat gtc aaa atg ttg       192
Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu
    50                  55                  60
aac gcc aag tcc att aac cac aag att agt agc ctt gct aaa ttt aat       240
Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn
65                  70                  75                  80
gaa ttt cta ata cag aaa gga agt caa caa gat caa gta att tta tta       288
Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu
                85                  90                  95
gat gta aaa aag ttt tta caa agt gtg tta gag gat aat aac aaa cgt       336
Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg
            100                 105                 110
aat tat gca att gcc act ctc cta gca tat aca gga gta cgt att tca       384
Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser
        115                 120                 125
gag gca tta tct atc aaa atg aat gac ttc aat tta cag act ggg gaa       432
Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu
    130                 135                 140
tgt att att cga agt gga aaa gga ggt aaa caa cga att gta tta cta       480
Cys Ile Ile Arg Ser Gly Lys Gly Gly Lys Gln Arg Ile Val Leu Leu
145                 150                 155                 160
aat agt aag gta ctt agt gct atc aaa gat tat ctc atc gat cga aaa       528
Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys
                165                 170                 175
aca tac agt aca gca cat gaa tct ccg tat ctt ttt att agt aaa aag       576
Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys
            180                 185                 190
cga gaa aag ctc gac cgt acg gtc gtc aat cgt atc ttt aaa tca tac       624
Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr
        195                 200                 205
agg aat gtt att act cca cac caa tta cga cac ttc ttc tgt acg aat       672
Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn
    210                 215                 220
gca att caa aaa gga ttt agc att cat gaa gtt gca aat caa gct ggg       720
Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly
225                 230                 235                 240
cac tct aac atc cat acg aca cta ctt tac aca aat cca aac caa ctg       768
His Ser Asn Ile His Thr Thr Leu Leu Tyr Thr Asn Pro Asn Gln Leu
                245                 250                 255
cag cta aaa aat aaa atg gag ctc tta taa                              798
Gln Leu Lys Asn Lys Met Glu Leu Leu
            260                 265
```

<210> 6

<211> 265
<212> PRT
<213> Bacillus thuringiensis

<400> 6
Met Asp Val Ala Lys Gln Phe Ser Ser Tyr Leu Lys Gln Glu Asn Lys
1 5 10 15

Thr Glu Asn Thr Val Gln Gly Tyr Thr Ser Gly Ile Arg Gln Tyr Ile
20 25 30

Lys Trp Phe Glu Gly Ser Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg
35 40 45

Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu
50 55 60

Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn
65 70 75 80

Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu
85 90 95

Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg
100 105 110

Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser
115 120 125

Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu
130 135 140

Cys Ile Ile Arg Ser Gly Lys Gly Gly Lys Gln Arg Ile Val Leu Leu
145 150 155 160

Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys
165 170 175

Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys
180 185 190

Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr
195 200 205

Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn
210 215 220

Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly
225 230 235 240

His Ser Asn Ile His Thr Thr Leu Leu Tyr Thr Asn Pro Asn Gln Leu
245 250 255

Gln Leu Lys Asn Lys Met Glu Leu Leu
260 265

<210> 7
<211> 116
<212> DNA
<213> Bacillus thuringiensis

<400> 7
taatacaaca caatattaat tgtgttgtat taggtgttat aataaatata tatctagggg 60
tttaacgcaa cacaatttat cgataaataa atacttttag acgcaacaca atttat 116

<210> 8
<211> 116
<212> DNA
<213> Bacillus thuringiensis

<400> 8
taatacaaca caatattaat tgtgttgtat taggtgttat aatatatata aatctagggg 60
tttaacgcaa cacaatttat cgataaataa atacttttag acgcaacaca atttat 116

<210> 9
<211> 116
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> N_region
<222> 33 .. 64
<223> n = a, t, g, or c

<220>
<221> N_region
<222> 81 .. 100
<223> n = a, t, g, or c

<400> 9
taatacaaca caatattaat tgtgttgtat tannnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnacgcaa cacaatttat nnnnnnnnnn nnnnnnnnnn acgcaacaca atttat 116

<210> 10
<211> 124
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> N_region
<222> 33 .. 74
<223> n = a, t, g, or c

<400> 10
taatacaaca caatattaat tgtgttgtat tannnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnacgcaa cacaatttac gataaataaa tacttttaga cgcaacacaa 120
ttta 124